

```
AMSH1.
                   ----MPDHIDVSLSPEERVRALSKIGCHITISEDITPRR 35
        MOO PTIVISLAKLAAMPOHIDVSLSPEERVRALSKIGCNITISEDITPRR 50
YN2H3
        -----NSDEGDVSLPPEDRVRALSQLGSAVEVNEDIPPRR 35
A MSH
                       YTR SOVEMERIAS VYLEE GHLEN A FVLYNK FIT LIVEK LPHIRDYOOC AV 85
AMSH1
        YTR SGVENERIAS VYLKE CHLENA FVLYNKTITLIVEK LENHRDYQQCAV 100
YN2H3
        YER SOVETTRIMAS TYSEE GNIEHAFT LYNKYTTLETEK LEKHROYKSAVI 85
A MSH
        AMSH1
        FERODINGELET AFFRIDELENDLIER YNVEYDEYLOSKNEYEREILEE 135
        PEKODINKKIKEI AFPRIDKIKNDLIKKYNVEYQEYIQSKNRYKAEILKK 150
AMSH2
HEMA
        FERROTVERIETATPRACEIKABLIERYTKEYTEYNEERKKEAEGIARN 135
        ANSH1
        LEHORLIE AKRKRIAOMROOOLK SEQILTITEDQ LKKOLLARGOMRSOOTS 185
        LEHORLIE AERKRIAOMROOOLE SEOFLIFFEDOLKKOELARGOMRSOOTS 200
MAI QQEEEKEKORVAOOROOOLE OEOTHAJEENIR MELEKERIKI VÕEF 185
YNZH3
AMSH
                                    **** ***** * ***
           ** ** ***** ***** ***
        d-leeqidgsalscfs--thomselhyfadopnksdatnyashsppynr 232
g-lseqidgsalscfs--thomselhyfadopnksdatnyashsppynr 247
THEMA
AMSH2
        GKVDPGLGGPLVPDLEKPSLDVFPTLTVSSIQPSDCRTTVRPAXPPVVDR 235
HEMA
             1, * - 1, 1, 1, 1, 1
                              ALTPATESAVON LANGUERCAA LIED CHRELOTAE SALAKOLI 383
AMSH1
AMSH2
        ALTPAATLSAVON LYVEGIRGVY LPEDICHRILOLAESNIVRGIETGGIL 29.7
AMSH-
        SIK PGALSNESI PTIDGIRHVV VPGRICPQTLQLASANTARGVETCGIL 285
                                   ** | ***** | ** | ** | ** | ** | ** | ** |
                     ***** ****
        CGK LITHIE FTITH VIVEN OSAGE DYCDHEN VEE LEN VOODHIDLITLIGH LEE 332
AMSHI
AMSH2
        CGK LITHIK FITTH VIVEX QSAGPDYCDMENVER LENVQDQHDLLTLGWIJJ 347
        CON LIMBRE PTITHIVLI EN OSAGS DYCHTENERE LE LIQUOGGLITICHI H 335.
AMSH
        THE TOTAL LESVELHIEC SYDIMLE ENTAINES PRENDICHTRICHAGML 382
AMSH1
       AMSH2
AMSH
        EVSACKKGTHPHIKEPRLFSICKHV--LVKDIKIIVLDLR--
AKSH1
        EVSACKROPHPHTKI PRLISIOKILSGIISGTALENT PLKIGYGPIGTP 447
AMSH2
        KISSCROKGTHPHSKDPPLFCSCSHVT--VVDRAVTITDLR------ 424
AMSH
        1 1 1
AMSH1
AMSH2
        LLGISRSSSPSEQL 461
AMSH
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COP9_su5 Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTOMLNOOFQEPFVAVVIDPTRTISAGKVNLG	
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVAIVVDPVRTVSAGKVCLG	
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLAVVIDPTRTVSAGKVEIG	
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVAIVIDPLRTMSAGKVDIG	
AF2198_Arcfu	LPIGMKVFGTVHSHPSPSCRPSEEDLSLFTRFGKYHIIVCYPYDENSWKCYNRKGEEV	
PH0451_Pyrho	MPHDESIKGTFHSHPSPFPYPSEGDLMFFSKFGGIHIIAAFPYDEDSVKAFDSEGREV	
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGYPYNLKDYSAYDRSGNKV	
MTH971 Metth	LPPFTGAVGSVHSHPGPVNLPSAADLHFFSKNGLFHLI IAHPYTMETVAAYTRNGDPV	
aq 1691 Aquae	ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYIIFSVQKGKVASYRSWELKGDKF	
RV1334_Myctu	EDADEVPVVI YHSHTATEAYPSRTDVKLATEPDAHYVLVSTRDPHRHELRSYRIVDGAVT	
RadC_Ecoli	IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDLRVLDHIVIGRGEYVSFA	

COP9 su5 Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTOMLNOOFQEPFVAVVIDPTRTISAGKVNLG	
COP9 su5 Dm	VGRMEHAVGWYHSHPGYGCWLSG1NVSTQMLNQTYQEPFVAIVVDPVRTVSAGKVCLG	
COP9 su5 At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLAVVIDPTRTVSAGKVBIG	
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVAIVIDPLRTMSAGKVDIG	
Padl Dm	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVAVVVDPIQSVKG-KVVID	
Padl Hs	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVAVVVDPIQSVKG-KVVID	
Sksl Dd	TGRDEIVIGWYHSHPGFGCWLSSVDVNTQQSFEQLQSRAVAVVVDPLQSVRG-KVVID	
Pad1_Sc	TGRDOMVVGWYHSHPGFGCWLSSVDVNTQKSFEQLNSRAVAVVVDPIQSVKG-KVVID	
HSHP '''''''''''''''''''''''''''''''''''		